

MAURER c
Ser. No. 09/111,866
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

1/28

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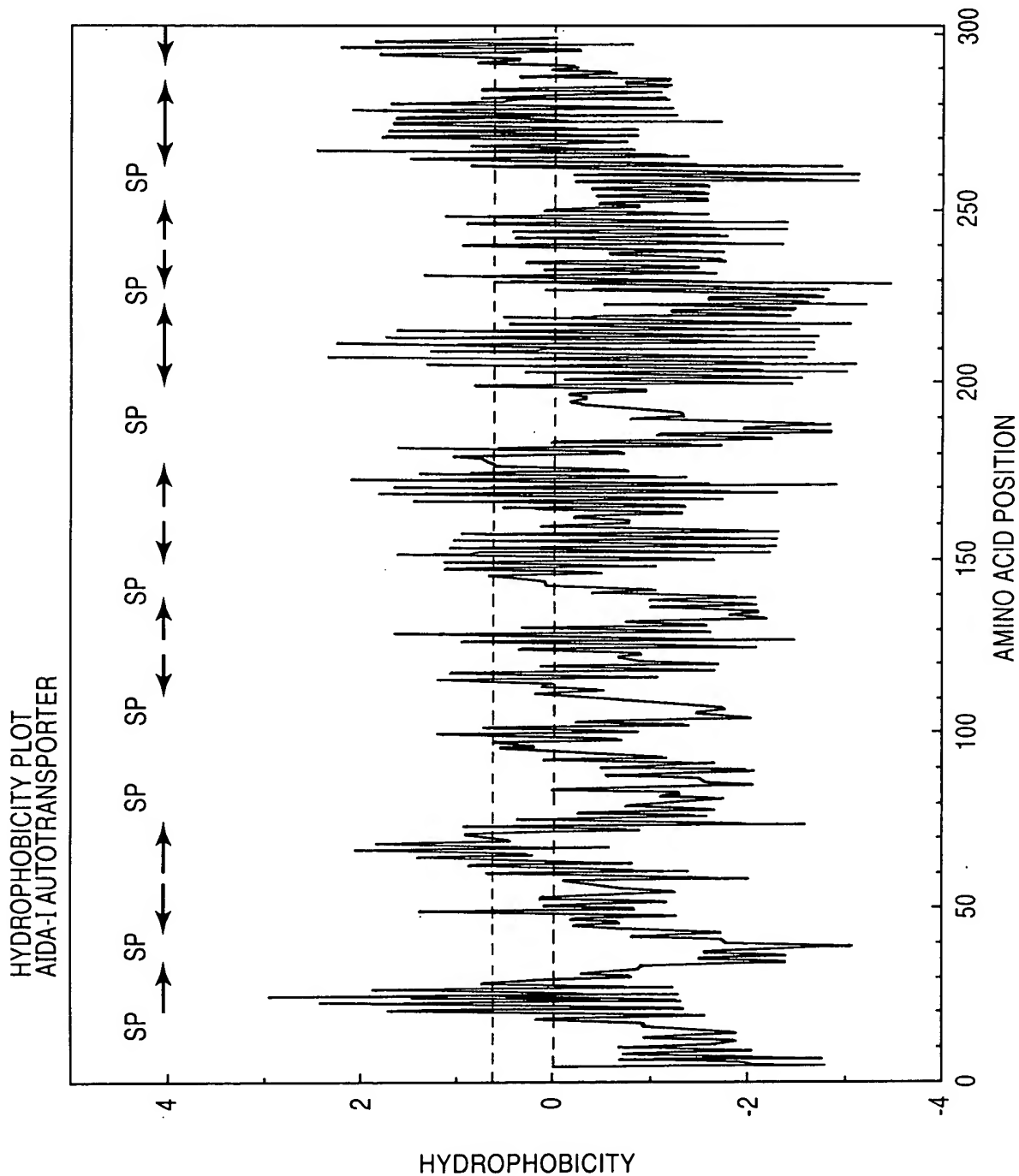
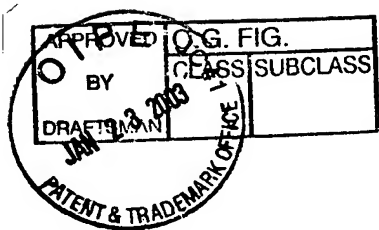


Fig.1

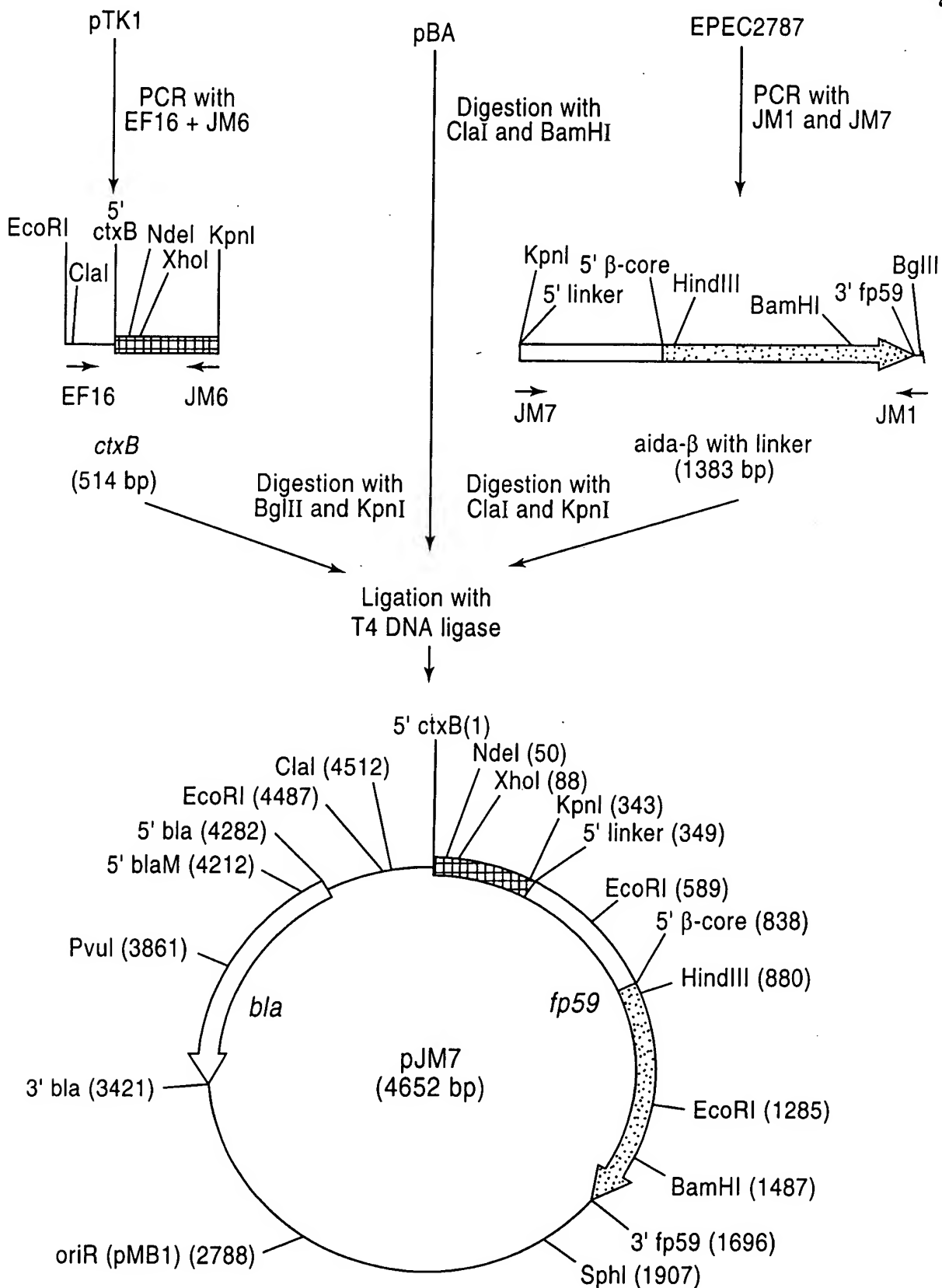


MAURILLO et al.
Ser. No. 09/47,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

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Fig.3a

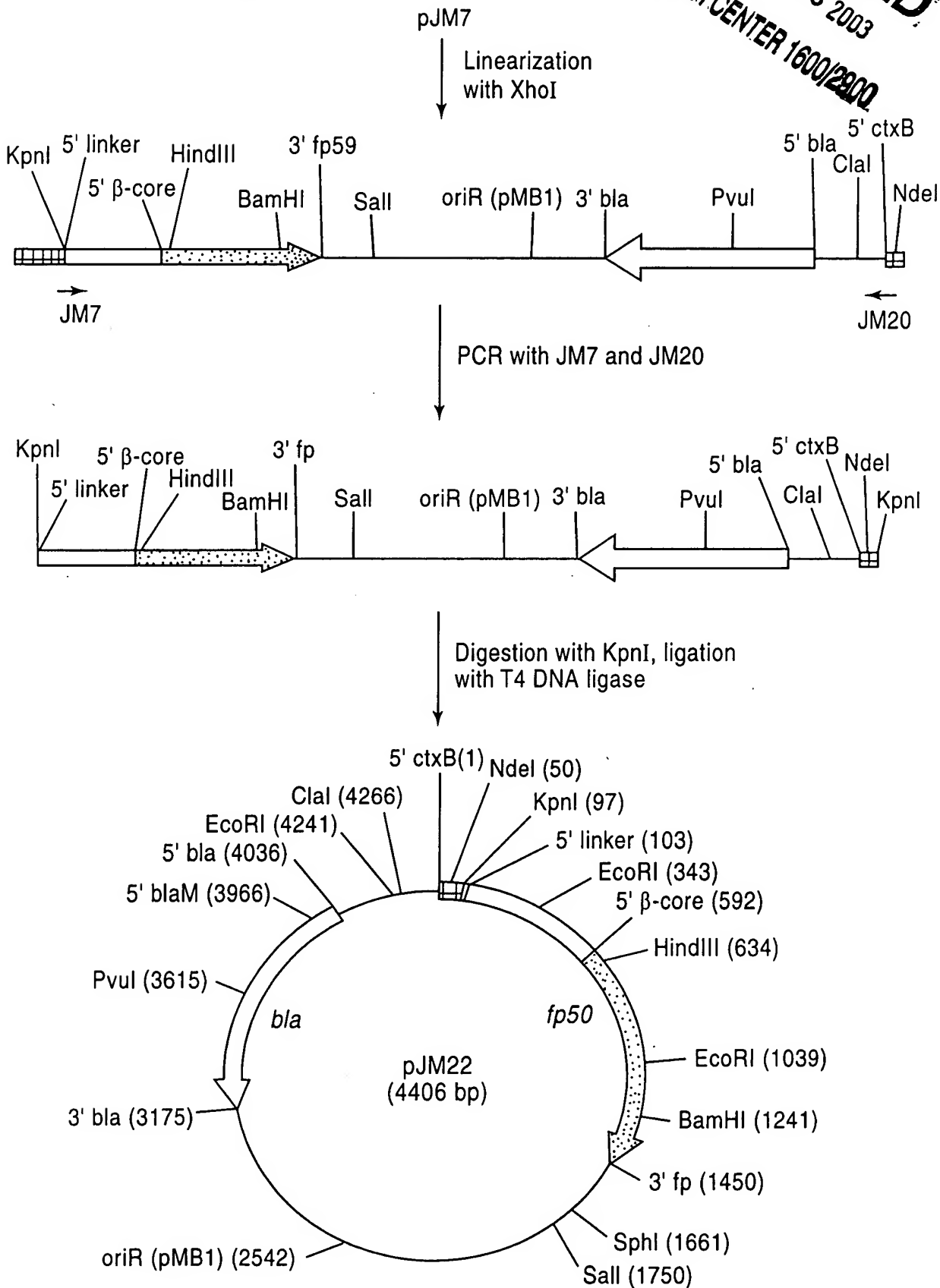
3/28

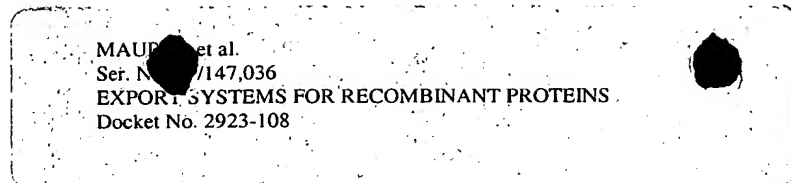
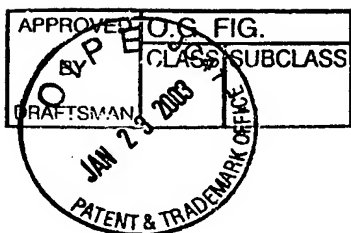


4/28

Fig.3b

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10/28

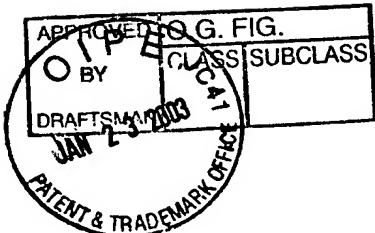


Fig.6

DNA sequences of the oligonucleotides used

Name	Use 1)	Length (bp)	Sequence (5'-3')
EF16	PCR (+)	36	TGTAAAACGACGGCCAGTATCACGAGG CCCTTTCGT
JM1	PCR (-)	27	GGAAGATCTGCCTCAGAAATGAGGGCC
JM6	PCR (-)	30	CATGGTACCAGGCGTTTTATTATTCCCT AC
JM7	PCR (+)	30	CGGGGTACCCTTAATCCTACAAAAGAA AGT
JM20	PCR (+)	44	AAGGGTACCTTTGAAATACTCCGGAGTA ATATTTTGTGAGGTGTTTC

1)
(+) and (-) relate to the coding (+) and the DNA strand
complementary thereto (-).



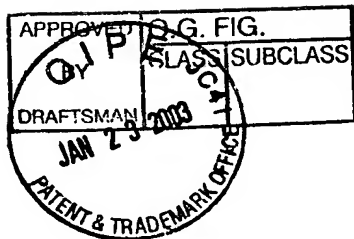
MAUREL et al.
Ser. No. 7,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

11/28

Fig.7

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GCATCCGTGTGGATGAAGATCACTGGAGGAATAAGCTCTGGTAAGCTTAATGACGGGCAA
1 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
A S V W M K I T G G I S S G K L N D G Q -
AATAAAACAACAACCAATCAGTTTATCAATCAGCTCGGGGGGATATTTATAAATTCCAT
61 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
N K T T T N Q F I N Q L G G D I Y K F H -
GCTGAACAACCTGGGTGATTTTACCTTAGGGATTATGGGAGGATACGCGAATGCAAAAGGT
121 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
A E Q L G D F T L G I M G G Y A N A K G -
AAAACGATAAATTACACGAGCAACAAAGCTGCCAGAAACACACTGGATGGTTATTCTGTC
181 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
K T I N Y T S N K A A R N T L D G Y S V -
GGGGTATACGGTACGTGGTATCAGAATGGGGAAAATGCAACAGGGCTCTTTGCTGAAACT
241 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
G V Y G T W Y Q N G E N A T G L F A E T -
TGGATGCAATATAACTGGTTTAATGCATCAGTGAAAGGTGACGGACTGGAAGAAGAAAAA
301 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
W M Q Y N W F N A S V K G D G L E E E K -
TATAATCTGAATGGTTTAACCGCTTCTGCAGGTGGGGGATATAACCTGAATGTGCACACA
361 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
Y N L N G L T A S A G G G Y N L N V H T -
TGGACATCACCTGAAGGAATAACAGGTGAATTCTGGTTACAGCCTCATTGTCAGGCTGTC
421 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
W T S P E G I T G E F W L Q P H L Q A V -
TGGATGGGGGTTACACCGGATACACATCAGGAGGATAACGGAACGGTGGTGCAGGGAGCA
481 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
W M G V T P D T H Q E D N G T V V Q G A -
GGGAAAAATAATATTTCAGACAAAAGCAGGTATTTCGTGCATCCTGGAAGGTGAAAAGCACC
541 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
G K N N I Q T K A G I R A S W K V K S T -
CTGGATAAGGATACCGGGCGGAGGTTCCGTCCGTATATAGAGGCAAACCTGGATCCATAAC
601 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
L D K D T G R R F R P Y I E A N W I H N -
ACTCATGAATTTGGTGTTAAAATGAGTGATGACAGCCAGTTGTTGTCAGGTAGCCGAAAT
661 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
T H E F G V K M S D D S Q L L S G S R N -
CAGGGAGAGATAAAGACAGGTATTGAAGGGGTGATTACTCAAACTTGTCAGTGAATGGC
721 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
Q G E I K T G I E G V I T Q N L S V N G -
GGAGTCGCATATCAGGCAGGAGGTACGGGAGCAATGCCATCTCCGGAGCACTGGGGATA
781 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
G V A Y Q A G G H G S N A I S G A L G I -
AAATACAGCTTC
841 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 852
K Y S F -



MAU et al.
Ser. No. 09/147,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

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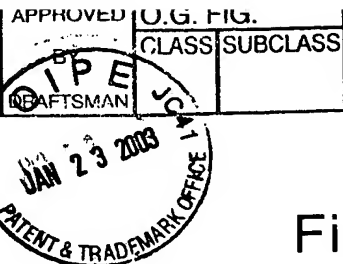
JAN 28 2003

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12/28

Fig.8

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CTGCGCCTGCGCGCCGACGCCGGCGGGCCATGGGCGCGTACGTTACGCGAGCGCCAGCAG
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
  L R L R A D A G G P W A R T F S E R Q Q -
ATCAGCAACCGCCACGCCCGCGCCTACGACCAGACGGTCAGCGGGCTGGAGATCGGCCTG
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
  I S N R H A R A Y D Q T V S G L E I G L -
GACCGTGGCTGGAGCGCGCTCGGGCGGGCGCTGGTACGCCGGCGGCCTGCTCGGCTACACC
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
  D R G W S A S G G R W Y A G G L L G Y T -
TATGCCGACCGCACCTATCCCGGCGACGGTGGCGGCAAGGTCAAGGGCCTGCACGTCGGC
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
  Y A D R T Y P G D G G G K V K G L H V G -
GGCTACGCCGCCTATGTGCGCGATGGCGGCTACTATCTCGACACCGTGCTGCGGCTGGGC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
  G Y A A Y V G D G G Y Y L D T V L R L G -
CGCTACGATCAGCAATACAACATTGCCGGCACCGATGGCGGGCCGCGTCACCGCCGACTAC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
  R Y D Q Q Y N I A G T D G G R V T A D Y -
CGCACAAGCGGCGCCGCATGGTCGCTCGAAGGCGGGCGCCGGTTCGAGCTGCCCAACGAC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
  R T S G A A W S L E G G R R F E L P N D -
TGGTTCGCCGAACCGCAGGCCGAGGTCATGCTGTGGCGCACGTCAGGCAAGCGCTATCGC
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
  W F A E P Q A E V M L W R T S G K R Y R -
GCCAGCAATGGCCTGCGCGTCAAGGTGGACGCCAACACCGCCACGCTGGGCGCGCCTGGGC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
  A S N G L R V K V D A N T A T L G R L G -
TTGCGCTTCGGCCGCGCATCGCCCTGGCCGGCGGCAACATCGTGACGCCCTACGCCAGG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
  L R F G R R I A L A G G N I V Q P Y A R -
CTCGGCTGGACGCAGGAGTTCAAAGCACGGGCGATGTGCGCACCAATGGCATTGGCCAT
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
  L G W T Q E F K S T G D V R T N G I G H -
GCCGGCGCAGGCCGCCACGGCCGCGTGGAACTGGGCGCGGGCGTCGACGCCCGCTTGGGC
661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
  A G A G R H G R V E L G A G V D A A L G -
AAGGGGCACAACCTCTATGCTTCGTACGAGTACGCGGCGGGCGACCGGATCAACATTCCG
721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
  K G H N L Y A S Y E Y A A G D R I N I P -
TGGTCGTTCCACGCCGGCTACCGCTACAGCTTC
781 -----+-----+-----+-----+-----+-----+-----+-----+ 813
  W S F H A G Y R Y S F -
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M. HIRER et al.
No. 09/147,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

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Fig.9

13/28

CAAAGCCTGTTTCGCATTAGAAAGCCGCACTTGAGGTTATTGATGCCCCACAGCAATCGGAA
1 Q S L F A L E A A L E V I D A P Q Q S E - 60
AAAGATCGTCTAGCTCAAGAAGAAGCGGAAAAACAACGCAAAACAAAAGACTTGATCAGC
61 K D R L A Q E E A E K Q R K Q K D L I S - 120
CGTTATTCAAATAGTGC GTTATCAGAATTATCTGCAACAGTAAATAGTATGCTTTCTGTT
121 R Y S N S A L S E L S A T V N S M L S V - 180
CAAGATGAATTAGATCGTCTTTTGTAGATCAAGCACAACTTGCCGTGTGGACAAATATC
181 Q D E L D R L F V D Q A Q S A V W T N I - 240
GCACAGGATAAAAGACGCTATGATTCTGATGCGTTCCGTGCTTATCAGCAGCAGAAAACG
241 A Q D K R R Y D S D A F R A Y Q Q Q K T - 300
AACTTACGTCAAATTGGGGTGCAAAAAGCCTTAGCTAATGGACGAATTGGGGCAGTTTTC
301 N L R Q I G V Q K A L A N G R I G A V F - 360
TCGCATAGCCGTTTCAGATAATACCTTTGATGAACAGGTTAAAAATCACGCGACATTAACG
361 S H S R S D N T F D E Q V K N H A T L T - 420
ATGATGTCGGGTTTTGCCCAATATCAATGGGGCGATTTACAATTTGGTGTAACGTGGGA
421 M M S G F A Q Y Q W G D L Q F G V N V G - 480
ACGGGAATCAGTGCAGTAAATGGCTGAAGAACAAGCCGAAAAATTCATCGAAAAGCG
481 T G I S A S K M A E E Q S R K I H R K A - 540
ATAAATTATGGCGTGAATGCAAGTTATCAGTTCCGTTTAGGGCAATTGGGCATTCAGCCT
541 I N Y G V N A S Y Q F R L G Q L G I Q P - 600
TATTTTGGAGTTAATCGCTATTTTATTGAACGTGAAAATTATCAATCTGAGGAAGTGAGA
601 Y F G V N R Y F I E R E N Y Q S E E V R - 660
GTGAAAACGCCTAGCCTTGCAATTTAATCGCTATAATGCTGGCATTCGAGTTGATTATACA
661 V K T P S L A F N R Y N A G I R V D Y T - 720
TTTACTCCGACAGATAATATCAGCGTTAAGCCTTATTTCTTCGTCAATTATGTTGATGTT
721 F T P T D N I S V K P Y F F V N Y V D V - 780
TCAAACGCTAACGTACAAACCACGGTAAATCTCACGGTGTTGCAACAACCATTGGACGT
781 S N A N V Q T T V N L T V L Q Q P F G R - 840
TATTGGCAAAAAGAAGTGGGATTAAAGGCAGAAATTTTACATTTCCAAATTTCCGCTTTT
841 Y W Q K E V G L K A E I L H F Q I S A F - 900
ATCTCAAAATCTCAAGGTTCACTCAACTCGGCAACAGCAAAATGTGGGCGTGAAATTGGGC
901 I S K S Q G S Q L G K Q Q N V G V K L G - 960
TATCGTTGG
961 Y R W - 969

17/28

Fig.13

1 CTGGGCGAGTTGCGCCTGAATCCGGACGCCGGCGGCTTGGGGCCGCGGCTTCGCGCAA 60
L G E L R L N P D A G G A W G R G F A Q -

61 CGCCAGCAACTGGACAACCGCGCGCGGGCGGCGCTTCGACCAGAAGGTGGCCGGCTTCGAG 120
R Q Q L D N R A G R R F D Q K V A G F E -

121 CTGGGCGCCGACCACGCGGTGGCGGTGGCCGGCGGGCGCTGGCACCTGGGCGGGCTGGCC 180
L G A D H A V A V A G G R W H L G G L A -

181 GGCTATACGCGCGCGACCGCGGCTTTACCGGCGACGGCGGGCCACACCGACAGCGTG 240
G Y T R G D R G F T G D G G G H T D S V -

241 CATGTCGGGGGCTATGCCACCTATATCGCCAACAGCGGTTTCTACCTGGACGCGACGCTG 300
H V G G Y A T Y I A N S G F Y L D A T L -

301 CGCGCCAGCCGCCTCGAAAATGACTTCAAGGTGGCGGGCAGCGATGGGTACGCGGTCAAG 360
R A S R L E N D F K V A G S D G Y A V K -

361 GGCAAGTACCGCACCCATGGGGTAGGCGTCTCGCTCGAGGCGGGCCGGCGCTTCGCCCAT 420
G K Y R T H G V G V S L E A G R R F A H -

421 GCCGACGGCTGGTTCCTCGAGCCGCGAGCCGAGCTGGCGGTGTTCCGGGTCGGCGGCGGT 480
A D G W F L E P Q A E L A V F R V G G G -

481 GCGTACCGCGCGGCCAATGGCCTGCGGGTGC GCGACGAAGGCGGCAGCTCGGTGCTGGGT 540
A Y R A A N G L R V R D E G G S S V L G -

541 CGCCTGGGCCTGGAGGTGCGCAAGCGCATCGAACTGGCAGGCGGCAGGCAGGTGCAGCCA 600
R L G L E V G K R I E L A G G R Q V Q P -

601 TACATCAAGGCCAGCGTGTTCAGGAGTTCGACGGCGCGGGTACGGTACGCACCAACGGC 660
Y I K A S V L Q E F D G A G T V R T N G -

661 ATCGCGCATCGCACCGAACTGCGCGGCACGCGCGCCGAAC TGGGCTGGGCATGGCCGCC 720
I A H R T E L R G T R A E L G L G M A A -

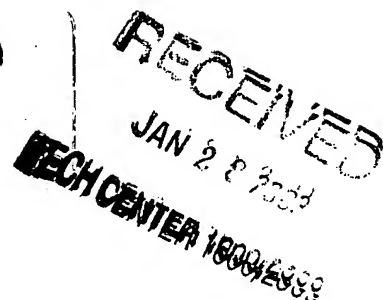
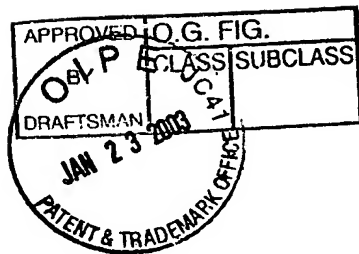
721 GCGCTGGGCGCGGCCACAGCCTGTATGCCTCGTACGAGTACTCCAAGGGCCCGAAGCTG 780
A L G R G H S L Y A S Y E Y S K G P K L -

781 GCCATGCCGTGGACCTTCCACGCGGGCTACCGGTACAGCTGG 822
A M P W T F H A G Y R Y S W -

18/28

Fig.14

1 AAGTTTGGTTCGCTGGATAAGCCCCGTTTGTCTCGGTAATGCAACGCAGAAGATGTGTAACAGT 60
K F G A W I S P F V G N A T Q K M C N S -
61 ATAAGTGGTTATAAGTCTGATACAACCTGGTGGCACTATAGGTTTTGACGGCTTCGTTAGC 120
I S G Y K S D T T G G T I G F D G F V S -
121 GATGATCTAGCACTCGGACTTGCATATACAAGAGCCGATACTGACATTAAGCTAAAAAAT 180
D D L A L G L A Y T R A D T D I K L K N -
181 AATAAAACGGGCGATAAGAATAAGGTAGAGAGCAACATCTATTCTTTATACGGTTTATAT 240
N K T G D K N K V E S N I Y S L Y G L Y -
241 AATGTACCTTATGAAAATCTCTTCGTTGAAGCTATAGCATCTTACTCAGATAATAAGATA 300
N V P Y E N L F V E A I A S Y S D N K I -
301 AGAAGCAAATCAAGACGTGTTATTGCAACGACACTAGAGACTGTCGGTTATCAAACCTGCA 360
R S K S R R V I A T T L E T V G Y Q T A -
361 AACGGTAAGTATAAATCCGAAAGCTATACAGGTCAGTTAATGGCTGGTTATACCTATATG 420
N G K Y K S E S Y T G Q L M A G Y T Y M -
421 ATGCCTGAGAACATTAACTTAACACCGCTAGCTGGGCTTAGATATTCGACTATCAAAGAT 480
M P E N I N L T P L A G L R Y S T I K D -
481 AAGGGCTATAAGGAAACCGGTACTACTTACCAAAATCTTACCGTTAAAGGCAAGAACTAT 540
K G Y K E T G T T Y Q N L T V K G K N Y -
541 AATACTTTTCGACGGTTTACTCGGTGCTAAAGTATCAAGTAATATCAATGTCAATGAAATA 600
N T F D G L L G A K V S S N I N V N E I -
601 GTGCTAACACCTGAGCTTTACGCAATGGTCGATTATGCATTCAAGAATAAAGTTTTCGGCG 660
V L T P E L Y A M V D Y A F K N K V S A -
661 ATTGATGCAAGGTTACAAGGTATGACTGCTCCTCTTCCAACCAACAGCTTTAAGCAAAGC 720
I D A R L Q G M T A P L P T N S F K Q S -
721 AAAACAAGTTTTGATGTCGGTGTCTGGTGTACTGCTAAGCATAAAATGATGGAATACAGG 780
K T S F D V G V G V T A K H K M M E Y R -
781 ATTAACCTACGATACCAATATCGGAAGTAAGTATTTTCGCTCAGCAAGGTAGTGTAAGTT 840
I N Y D T N I G S K Y F A Q Q G S V K V -
841 CGTGTTAATTTT 852
R V N F -



19/28

Fig.15

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1  TCTTATGGTGTATGGGCTAAACCTTTCTATAACATTGCAGAACAAGACAAAAAGGTGGT 60
   S Y G V W A K P F Y N I A E Q D K K G G -
61  ATAGCTGGTTATAAAGCAAAACTACTGGGGTTGTAGTTGGTTAGATACTCTCGCTAGC 120
   I A G Y K A K T T G V V V G L D T L A S -
121 GATAACCTAATGATTGGGGCAGCTATTGGGATCACTAAAACGATATAAAACACCAAGAT 180
   D N L M I G A A I G I T K T D I K H Q D -
181 TATAAGAAAGGTGATAAACTGATATTAATGGTTTATCATTCTCTCTATATGGTTCCCAA 240
   Y K K G D K T D I N G L S F S L Y G S Q -
241 CAGCTTGTTAAGAATTTCTTTGCTCAAGGTAATTCAATCTTTACCTTAAACAAAGTCAAA 300
   Q L V K N F F A Q G N S I F T L N K V K -
301 AGTAAAAGTCAGCGTTACTTCTTCGAGTCTAATGGTAAGATGAGCAAGCAAATTGCTGCT 360
   S K S Q R Y F F E S N G K M S K Q I A A -
361 GGTAATTACGATAACATGACATTTGGTGGTAATTTAATATTTGGTTATGATTATAATGCA 420
   G N Y D N M T F G G N L I F G Y D Y N A -
421 ATGCCAAATGTATTAGTAACCTCCAATGGCAGGACTTAGCTACTTAAAATCTTCTAATGAA 480
   M P N V L V T P M A G L S Y L K S S N E -
481 AATTATAAAGAAACCGGTACAACAGTTGCAAATAAGCGCATTAAATAGCAAATTTAGTGAT 540
   N Y K E T G T T V A N K R I N S K F S D -
541 AGAGTCGATTTAATAGTAGGGGCTAAAGTAGCTGGTAGTACTGTGAATATAACTGATATT 600
   R V D L I V G A K V A G S T V N I T D I -
601 GTGATATATCCGGAAATTCATTCTTTTGTGGTGCACAAAGTAAATGGTAAATTATCTAAC 660
   V I Y P E I H S F V V H K V N G K L S N -
661 TCTCAGTCTATGTTAGATGGACAAACTGCTCCATTTATCAGTCAACCTGATAGAACTGCT 720
   S Q S M L D G Q T A P F I S Q P D R T A -
721 AAAACGTCTTATAATATAGGCTTAAGTGCAAACATAAAATCTGATGCTAAGATGGAGTAT 780
   K T S Y N I G L S A N I K S D A K M E Y -
781 GGTATCGGTTATGATTTTAATTCTGCAAGTAAATATACTGCACATGAAGGTACTTTAAAA 840
   G I G Y D F N S A S K Y T A H Q G T L K -
841 GTACGTGTAACTTC 855
   V R V N F -

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20/28

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Fig.16

1 GCTTACGGTATATGGGCAAAACCTTTCTATACTGATGCACATCAAAGTAAGAAAGGTGGT 60
A Y G I W A K P F Y T D A H Q S K K G G -

61 TTAGCTGGTTATAAAGCTAAAACCACCGGTGTCGTAATCGGTTTAGATACGCTAGCTAAC 120
L A G Y K A K T T G V V I G L D T L A N -

121 GATAATTTAATGATCGGTGCTGCTATCGGTATCACTAAAACCTGATATAAAACATCAAGAT 180
D N L M I G A A I G I T K T D I K H Q D -

181 TATAAGAAAGGTGATAAAACCGACGTTAACGGTTTCTCATTCTCTCTATATGGTGCCAG 240
Y K K G D K T D V N G F S F S L Y G A Q -

241 CAGCTTGTTAAGAAGCTTCTTTGCTCAAGGTAGTGCAATATTTAGCTTAAACCAAGTGAAG 300
Q L V K N F F A Q G S A I F S L N Q V K -

301 AACAAAAGTCACGGTTACTTCTTCGATGCTAACGGTAATATGAGCAAGCAAATTGCTGCC 360
N K S Q R Y F F D A N G N M S K Q I A A -

361 GGTCATTACGATAACATGACATTTGGTGGTAACTTAACAGTCGGTTATGATTACAATGCA 420
G H Y D N M T F G G N L T V G Y D Y N A -

421 ATGCAAGGTGTGTTAGTAAGTCCAATGGCAGGACTTAGCTACTTAAAGTCTTCTGACGAA 480
M Q G V L V T P M A G L S Y L K S S D E -

481 AACTACAAAGAAACCGGTACAACAGTTGCAAACAAGCAAGTTAACAGCAAATTTAGCGAT 540
N Y K E T G T T V A N K Q V N S K F S D -

541 AGAACCGATTTAATAGTAGGTGCTAAAGTAGCCGGCAGTACTATGAACATAACTGATCTT 600
R T D L I V G A K V A G S T M N I T D L -

601 GCGGTATATCCAGAAGTTCACGCTTTTGTGGTTTCAAAAGTAACCGGTAGATTATCTAAA 660
A V Y P E V H A F V V H K V T G R L S K -

661 ACTCAGTCTGTATTAGACGGACAAGTTACTCCGTGTATCAACCAGCCTGACAGAACCACT 720
T Q S V L D G Q V T P C I N Q P D R T T -

721 AAAACATCTTATAATTTAGGTTTAAGTGCAAGCATAAGATCTGATGCTAAGATGGAGTAC 780
K T S Y N L G L S A S I R S D A K M E Y -

781 GGAATCGGTTACGATGCTCAGATTTCAAGTAAATATACTGCACATCAAGGTACTCTAAAA 840
G I G Y D A Q I S S K Y T A H Q G T L K -

841 GTCCGTGTAACTTC 855
V R V N F -

APPROVED O.G. FIG.
BY CLASS SUBCLASS
DRAFTSMAN
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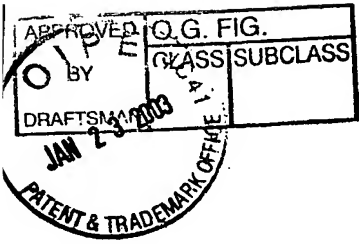
MAU et al.
Ser. 9/147,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108


21/28

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Fig.17

1 TCTTATGGTGTATGGGCTAAACCTTTCTATAACATCGCAGAACAAAGATAAAAAAGGTGGT 60
S Y G V W A K P F Y N I A E Q D K K G G -
61 CTAGCTGGTTATAAAGCAAAAAGTCTGGTGTGTAGTTGGTTTAGATACTCTCGCTAAT 120
L A G Y K A K T A G V V V G L D T L A N -
121 GATAACCTAATGATTGGTGCAGCTATTGGTATCACTAAAGTACATAAAACACCAAGAT 180
D N L M I G A A I G I T K T D I K H Q D -
181 TATAAAAAAGGTGATAAAAGTATTAAGGGTTTATCCTTCTCTCTATATGGTGCCCAG 240
Y K K G D K T D I K G L S F S L Y G A Q -
241 CAGCTTGTTAAGAATTTCTTTGCTCAAGGTAGTGCAATATTTACCTTAAACAAAGTCAAA 300
Q L V K N F F A Q G S A I F T L N K V K -
301 AGTAAAAGTCAGCGTTACTTCTTCGATGCTAATGGTAAGATGAACAAGCAAATTGCTGCC 360
S K S Q R Y F F D A N G K M N K Q I A A -
361 GGTAATTATGATAACATAACATTCGGTGGTAATTTAATGTTTGGTTATGATTATAATGCA 420
G N Y D N I T F G G N L M F G Y D Y N A -
421 CTGCAAGGTGTATTAGTGACTCCAATGGCAGGGCTTAGCTACTTAAATCTTCTAATGAA 480
L Q G V L V T P M A G L S Y L K S S N E -
481 AACTATAAAGAACTGGTACTACAGTTGCAAATAAGCGCATTACAGCAAATTTAGTGAT 540
N Y K E T G T T V A N K R I H S K F S D -
541 AGAATCGATTTAATAGTAGGTGCTAAAGTAACTGGTAGTGCTATGAATATAAATGATATT 600
R I D L I V G A K V T G S A M N I N D I -
601 GTGATATATCCAGAAATTCATTCTTTGTAGTGACAAAGTAAATGGTAAGCTATCTAAG 660
V I Y P E I H S F V V H K V N G K L S K -
661 GCTCAGTCTATGTTAGATGGACAAAGTCTCCATTTATCAGTCAGCCTGATAGAAGTCTG 720
A Q S M L D G Q T A P F I S Q P D R T A -
721 AAAACATCTTATAATATAGGCTTAAGTGCAAATATAAGATCTGATGCTAAGATGGAGTAT 780
K T S Y N I G L S A N I R S D A K M E Y -
781 GGTATCGGTTATGATTTTAATGCTGCAAGTAAATATACTGCACATCAAGGTACTTTAAAA 840
G I G Y D F N A A S K Y T A H Q G T L K -
841 GTACGTATAAATTTTC 855
V R I N F -



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Ser. No. 09/147,036
EXPORT SYSTEMS FOR RECOMBINANT PROTEINS
Docket No. 2923-108

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22/28

Fig.18

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CAGGGGGATGCCGGTGTCTGGGCACGCATAATGAATGGTACCGGTTCCGGCAGATGGTGAC
1  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
  Q G D A G V W A R I M N G T G S A D G D -

TACAGCGATAACTACACTCACGTTTCAGATTGGTGTCGACAGAAAAGCATGAGCTGGACGGT
61  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
  Y S D N Y T H V Q I G V D R K H E L D G -

GTGGATTTATTTACGGGGGCATTGCTGACCTATACGGACAGCAATGCAAGCAGCCACGCA
121  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
  V D L F T G A L L T Y T D S N A S S H A -

TTCAGTGGAAAAACAAATCCGTGGGTGGCGGTCTGTATGCCTCTGCACTCTTTAATTCC
181  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
  F S G K N K S V G G G L Y A S A L F N S -

GGAGCTTATTTTGACCTGATTGGTAAATATCTCCATCATGATAATCAGCACACGGCGAAT
241  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
  G A Y F D L I G K Y L H H D N Q H T A N -

TTTGCCTCACTGGGAACAAAAGACTACAGCTCTCATTCCTGGTATGCCGGTGCTGAAGTT
301  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
  F A S L G T K D Y S S H S W Y A G A E V -

GGTTATCGTTACCACCTGACGAAAGAGTCCTGGGTGGAGCCACAGATAGAGCTGGTTTAC
361  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
  G Y R Y H L T K E S W V E P Q I E L V Y -

GGTTCTGTATCAGGAAAAGCTTTTAGCTGGGAAGCCCGGGAATGGCTCTGAGCATGAAA
421  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
  G S V S G K A F S W E A R G M A L S M K -

GACAAGGATTATAACCCACTGATTGGCCGTACTGGTGTGACGTGGGAAGAGCCTTCTCC
481  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
  D K D Y N P L I G R T G V D V G R A F S -

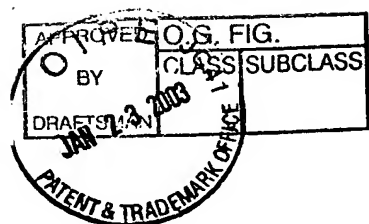
GGAGACGACTGGAAAATCACAGCTCGAGCCGGGCTGGGTTATCAGTTTCGACCTGCTGGCG
541  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
  G D D W K I T A R A G L G Y Q F D L L A -

AACGGAGAAACGGTTCTGCAGGATGCTTCCGGAGAGAAACGTTTCGAAGGTGAAAAAGAT
601  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
  N G E T V L Q D A S G E K R F E G E K D -

AGCAGGATGCTGATGACGGTAGGGATGAATGCCGAAATTAAGGATAATATGCGTTTGGGA
661  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
  S R M L M T V G M N A E I K D N M R L G -

CTGGAGCTGGAGAAATCAGCGTTCGGGAAATATAATGTGGATAATGCGATAAACGCCAAC
721  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
  L E L E K S A F G K Y N V D N A I N A N -

TTCCGTTATGTTTTC
781  -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 795
  F R Y V F -
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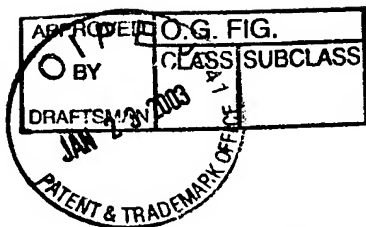


23/28

Fig.19

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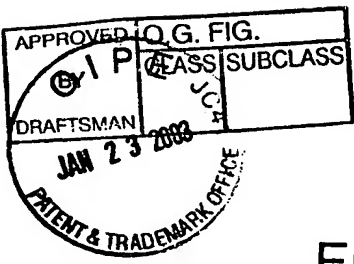
1 ACCCGTCAACTGTCCGGCCAGATCCACGCGGATATGGCGTCCGCCAGATTAAACG
T R Q L S G Q I H A D M A S A Q I N E S -
61 CGTTATCTGCGCGATACCGCCACCGAGCGGTTGCGCCAGGCCGATGGCCGCCGCACCGCT
R Y L R D T A T E R L R Q A D G R R T A - 120
121 TCCGATATCAAAGCGGATGATAATGGCGCCTGGGCGAAATTGCTGGGCAACTGGGGGCAT
S D I K A D D N G A W A K L L G N W G H - 180
181 GCTTCCGGCAACGACAACGCTACCGGTTACCAGACATCCACCTATGGCGTGCTGTTGGGT
A S G N D N A T G Y Q T S T Y G V L L G - 240
241 CTGGACAGCGAACTGTTTGACGACGGCCGGCTGGGCGTGATGACCGGGTATACCCGCACG
L D S E L F D D G R L G V M T G Y T R T - 300
301 TCGCTGGTAGGCGGTCTACAGTCAGTAGTCCACAGCGACACTACACATCTGGGGCTGTAC
S L V G G L Q S V V H S D T T H L G L Y - 360
361 GGCGACAAACGCTTCGGCGCGTTGGCGCTGCCAGCGGGCGGCACCTATACCTGGCATCGC
G D K R F G A L A L P A G G T Y T W H R - 420
421 ATCGACACGTCGCGCTCGGTAAACTACGGCGCGCAGGCGGATCGCGAAAAGGCCCGCTAT
I D T S R S V N Y G A Q A D R E K A R Y - 480
481 AACGCGCGCACCGGTCAGCTGTTTATCGAAAGCGGCTACGATTGGAGCAACGACGTGGTC
N A R T G Q L F I E S G Y D W S N D V V - 540
541 AATCTTGAGCCGTTCCGCAACCTGGCGTACACCCACTATCGCAACGAGGGGATCAACGAG
N L E P F A N L A Y T H Y R N E G I N E - 600
601 CAAGGCGGGGCGGCGCGCTGCGCGGCGATAAGCAAAGTCAGTCCGCCACCGCTTCGACG
Q G G A A A L R G D K Q S Q S A T A S T - 660
661 CTGGGCCTGCGCGCCGATACGCAATGGCAGACCGACAGCGTGGCGATCGCCCTGCCGGGC
L G L R A D T Q W Q T D S V A I A L P G - 720
721 GAGCTGGGTTGGCAACATCAGTACGGCAAGCTGGAGCGTAAAACACAGCTGATGTTCAA
E L G W Q H Q Y G K L E R K T Q L M F K - 780
781 CGCAGCGATGTCGCGTTCGACGTGAACAGCGTCCCTGTTTCTCGCGATGGGGCCATTCTG
R S D V A F D V N S V P V S R D G A I L - 840
841 AAAGCGGGCGTCGATGTATCGATTAAACAAAACGTCGTCCTGTCCCTTGGGTACGGCGGG
K A G V D V S I N K N V V L S L G Y G G - 900
901 CAGCTGTCGTCCAACCACCAGGACAACAGCGTCAACGCCGGCCTGACCTGGCGGTTTC
Q L S S N H Q D N S V N A G L T W R F - 957



24/28

Fig.20

ACCCGTCAACTGTCCGGCCAGATCCACGCGGATATGGCTTCCGCCCAGATCAACGAAAGC
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
T R Q L S G Q I H A D M A S A Q I N E S -
CGTTACCTGCGCGATACCGCCACCGAGCGCTTGCGCCAGGCGGAAGGCCGCCGACCGCT
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
R Y L R D T A T E R L R Q A E G R R T A -
ACCGACATTAAAGCGGATGACAACGGCGCCTGGGCGAAACTGCTGGGTAGCTGGGGGCAT
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
T D I K A D D N G A W A K L L G S W G H -
GCTTCCGGCAACGACAACGCCACCGGTTACCAGACCTCCACCTATGGCGTGCTGTTAGGT
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
A S G N D N A T G Y Q T S T Y G V L L G -
CTGGACAGCGAACTGTTTGGCGACGGCGGCTTGGCATGATGACCGGGTATACCCGCACT
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
L D S E L F G D G R L G M M T G Y T R T -
TCGCTGGATGGAGGTTATCAGTCAGATGCTCACAGCGACAACCTACCATCTGGGGCTGTAC
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
S L D G G Y Q S D A H S D N Y H L G L Y -
GGCGACAAACGCTTCGGCGCGTTGGCGCTGCGAGCGGGCGGCACCTATACCTGGCATCGC
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
G D K R F G A L A L R A G G T Y T W H R -
ATCGACACCTCGCGTTCCGTTGAACCTACGGCGCGCAGTCGGATCGCGAGAAGGCCAAGTAT
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
I D T S R S V N Y G A Q S D R E K A K Y -
AACGCGCGCACCGGTCAGCTGTTTCATCGAAAGCGGCTACGATTGGACGAGCGATGCGGTC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
N A R T G Q L F I E S G Y D W T S D A V -
AACCTTGAGCCGTTCCGCAACCTGGCGTATACCCATTACCGTAACGAGGAGATCAACGAG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
N L E P F A N L A Y T H Y R N E E I N E -
CAAGGCGGGGCAGCGGCGCTGCGCGGCGACAAACAAAGTCAGTCCGCCACCGCCTCGACG
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
Q G G A A A L R G D K Q S Q S A T A S T -
TTGGGTCTGCGCGCCGACACCGAGTGGCAAACCGACAGCGTGGCGATCGCGCTGCGCGGC
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
L G L R A D T E W Q T D S V A I A L R G -
GAGCTGGGTTGGCAGCATCAGTACGGCAAGCTGGAGCGTAAAACGCAGCTGATGTTCAAA
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
E L G W Q H Q Y G K L E R K T Q L M F K -
CGCACTGATGCGGCGTTCGACGTGAACAGCGTGCCTGTTTCTCGCGATGGCGCGATTCTG
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
R T D A A F D V N S V P V S R D G A I L -
AAAGCGGGCGTCGATGTATCGATTAAACAAAACGCCGTCCTGTCCCTTGGCTACGGCGGG
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
K A G V D V S I N K N A V L S L G Y G G -
CAGCTGTCGTCCAACCACCAGGACAACAGCGTCAACGCCGGTCTGACCTGGCGCTTC
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 957
Q L S S N H Q D N S V N A G L T W R F -



25/28

Fig.21

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1  TTCCGTCAGCTGTCGGGGCAAATCCATGCGGACATCGCGTCGGCGCTGGTGAACGACAGC 60
   F R Q L S G Q I H A D I A S A L V N D S -
61  CGCTACCTGCGTGAGGCGCTGAACGGGCGTCTGCGTCAGGCGGAAGGGCTGGCGAGCTCG
   R Y L R E A L N G R L R Q A E G L A S S -
121 TCGGCCATCAAGGCGGACGAGGACGGCGCCTGGGCGCAGCTGCTGGGAGCGTGGGACCAT
   S A I K A D E D G A W A Q L L G A W D H -
181 GCGTCGGGCGACGCCAACGCCACCGGCTATCAGGCCTCGACCTACGGGGTGCTGGTGGGG
   A S G D A N A T G Y Q A S T Y G V L V G -
241 CTGGACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
   L D S A A A A D W R L G V A T G Y T R T -
301 TCGCTGCACGGCGGGTATGGGTGCAAGGCGGACAGCGACAACCTACCACCTGGCGGCGTAC
   S L H G G Y G S K A D S D N Y H L A A Y -
361 GCGGACAAGCAGTTCGGGGCGCTGGCGCTGCGGGGCGGGGCGGGGCTACACCTGGCACCGC
   G D K Q F G A L A L R G G A G Y T W H R -
421 ATCGACACCAAGCGGTTCGGTGAACCTACGGGATGCAGTCGGACCGCGACACGGCGAAGTAC
   I D T K R S V N Y G M Q S D R D T A K Y -
481 AGCGCGCGCACCGAGCAGCTGTTTCGCGGAAGCGGGCTACAGCGTGAAGGGCGAGTGGCTG
   S A R T E Q L F A E A G Y S V K G E W L -
541 AACCTGGAGCCGTTTCGTCAACCTGGCGTACGTGAACTTTGAAAACAACGGCATCGCGGAA
   N L E P F V N L A Y V N F E N N G I A E -
601 AGCGGCGGCGCAGCGGCGCTGCGCGGCGACAAGCAGCACACCGACGCGACGGTGTTCGACG
   S G G A A A L R G D K Q H T D A T V S T -
661 CTGGGACTGCGCGCGGACACTGAGTGGCAGGTGAGCCCGGGCACGACGGTGGCGCTGCGC
   L G L R A D T E W Q V S P G T T V A L R -
721 AGCGAGCTGGGGTGGCAACACCAGTACGGCGGGCTGGAGCGTGGCACCGGGCTGCGGTTC
   S E L G W Q H Q Y G G L E R G T G L R F -
781 AACGGCGGCAACGCGCGGTTTCGTGGTGGACAGCGTGCCGGTGTGCGCGGACGGGATGGTG
   N G G N A P F V V D S V P V S R D G M V -
841 CTGAAGGCGGGTGCAGGAAGTGGCGGTGAACGAGAACGCCTCGCTGTGCTGGGCTACGGC
   L K A G A E V A V N E N A S L S L G Y G -
901 GGGCTGCTGTGCGCAGAACCATCAGGACAACAGCGTCAACGCCGGCTTCACCTGGCGCTTC
   G L L S Q N H Q D N S V N A G F T W R F -

```

Fig.22

26/28

1 TTCCGTCAGCTGTCGGGGCAAATCCATGCGGACATCGCGTCGGCGCTGGTGAACGACAGC 60
 F R Q L S G Q I H A D I A S A L V N D S -

61 CGCTACCTGCGTGAGGCGCTGAACGGGCGTCTGCGTCAGGCGGAAGGGCTGGCGAGCTCG 120
 R Y L R E A L N G R L R Q A E G L A S S -

121 TCGGCCATCAAGGCGGACGAGGACGGCGCCTGGGCGCAGCTGCTGGGAGCGTGGGACCAT 180
 S A I K A D E D G A W A Q L L G A W D H -

181 GCGTCGGGCGACGCCAACGCCACCGGCTATCAGGCCTCGACCTACGGGGTGCTGGTGGGG 240
 A S G D A N A T G Y Q A S T Y G V L V G -

241 CTGGACTCGGCGGCGGCGGCGGCGGCTGGGGGTGGCGACCGGCTACACCGGCACC 300
 L D S A A A A D W R L G V A T G Y T R T -

301 TCGCTGCACGGCGGGTATGGGTGCAAGGCGGACAGCGACAACCTACCACCTGGCGGCGTAC 360
 S L H G G Y G S K A D S D N Y H L A A Y -

361 GGCGACAAGCAGTTCTGGGGCGCTGGCGCTGCGGGGCGGGCGGGCTACACCTGGCACC GC 420
 G D K Q F G A L A L R G G A G Y T W H R -

421 ATCGACACCAAGCGGTCTGGTGAACCTACGGGATGCAGTCGGACCGCGACACGGCGAAGTAC 480
 I D T K R S V N Y G M Q S D R D T A K Y -

481 AGCGCGCGCACCGAGCAGCTGTTCGCGGAAGCGGGCTACAGCGTGAAGGGCGAGTGGCTG 540
 S A R T E Q L F A E A G Y S V K G E W L -

541 AACCTGGAGCCGTTCTGTAACCTGGCGTACGTGAACTTTGAAAACAACGGCATCGCGGAA 600
 N L E P F V N L A Y V N F E N N G I A E -

601 AGCGGCGGCGCAGCGGCGCTGCGCGGCGACAAGCAGCACACCGACGCGACGGTGTGACG 660
 S G G A A A L R G D K Q H T D A T V S T -

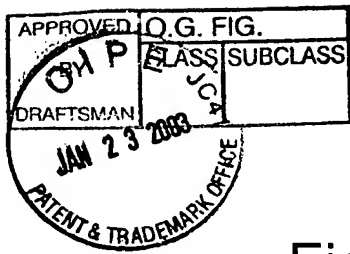
661 CTGGGACTGCGCGCGGACACTGAGTGGCAGGTGAGCCCGGGCACGACGGTGGCGCTGCGC 720
 L G L R A D T E W Q V S P G T T V A L R -

721 AGCGAGCTGGGGTGGCAACACCAGTACGGCGGGCTGGAGCGTGGCACCGGGCTGCGGTTC 780
 S E L G W Q H Q Y G G L E R G T G L R F -

781 AACGGCGGCAACGCGCCGTTCTGTGGTGGACAGCGTGCCGGTGTGCGCGGACGGGATGGTG 840
 N G G N A P F V V D S V P V S R D G M V -

841 CTGAAGGCGGGTGGGAAGTGGCGGTGAACGAGAACGCCCTGCTGTGCTGGGCTACGGC 900
 L K A G A E V A V N E N A S L S L G Y G -

901 GGGCTGCTGTCGAGAACCATCAGGACAACAGCGTCAACGCCGGCTTCACCTGGCGCTTC 960
 G L L S Q N H Q D N S V N A G F T W R F -



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Docket No. 2923-108

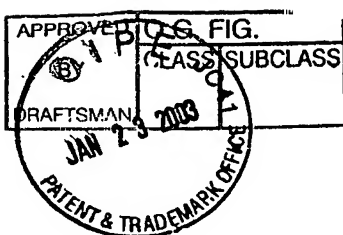
27/28

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Fig.23

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1  ATTAATGGCGAAGCCCGGTACGTGGGTGCGTCTGCTGAACGGTTCCGGCTCTGCTGATGGC 60
   I N G E A G T W V R L L N G S G S A D G -
61  GGTTCCTACTGACCACTATACCCTGCTGCAGATGGGGGCTGACCGTAAGCACGAACTGGGA 120
   G F T D H Y T L L Q M G A D R K H E L G -
121 AGTATGGACCTGTTTACCGGCGTGATGGCCACCTACACTGACACAGATGCGTCAGCAGAC 180
   S M D L F T G V M A T Y T D T D A S A D -
181 CTGTACAGCGGTAAACAAAATCATGGGGTGGTGGTTTCTATGCCAGTGGTCTGTTCCGG 240
   L Y S G K T K S W G G G F Y A S G L F R -
241 TCCGGCGCTTACTTTGATGTGATTGCCAAATATATTACAAATGAAAACAAATATGACCTG 300
   S G A Y F D V I A K Y I H N E N K Y D L -
301 AACTTTGCCGGAGCTGGTAAACAGAACTTCCGCAGCCATTCACTGTATGCAGGTGCAGAA 360
   N F A G A G K Q N F R S H S L Y A G A E -
361 GTCGGATACCGTTATCATCTGACAGATACGACGTTTGTGTAACCTCAGGCGGAACCTGGTC 420
   V G Y R Y H L T D T T F V E P Q A E L V -
421 TGGGGAAGACTGCAGGGCCAAACATTTAACTGGAACGACAGTGAATGGATGTCTCAATG 480
   W G R L Q G Q T F N W N D S G M D V S M -
481 CGTCGTAACAGCGTTAATCCTCTGGTAGGCAGAACCGGCGTTGTTTCCGGTAAACCTTC 540
   R R N S V N P L V G R T G V V S G K T F -
541 AGTGGTAAGGACTGGAGTCTGACAGCCCGTGCCGGCCTGCATTATGAGTTTCGATCTGACG 600
   S G K D W S L T A R A G L H Y E F D L T -
601 GACAGTCTGACGTTTCATCTGAAGGATGCAGCGGGAGAACATCAGATTAATGGCAGAAAA 660
   D S A D V H L K D A A G E H Q I N G R K -
661 GACAGTCGTATGCTTTACGGTGTGGGGTTAAATGCCCCGTTTGGCGACAATACGCGTTTG 720
   D S R M L Y G V G L N A R F G D N T R L -
721 GGGCTGGAAGTTGAACGCTCTGCATTGTTGTAATACAACACAGATGATGCGATAAACGCT 780
   G L E V E R S A F G K Y N T D D A I N A -
781 AATATTCGTTATTCATTC 798
   N I R Y S F -
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28/28

Fig.24

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1  TCTTTAGAAAGCGCGGCGGAAGTGTGTATCAATTTGCCCTAAATATGAAAAACCCACC
   S L E S A A E V L Y Q F A P K Y E K P T 60
61  AATGTTTCGCTAACGCTATTGGGGGAACGAGCTTGAATAGTGGCGGTAACGCTTCATTG
   N V W A N A I G G T S L N S G G N A S L 120
121 TATGGCACAAGTGC GGGCGTAGATGCTTACCTTAACGGGGAAGTGAAGCCATTGTGGGC
   Y G T S A G V D A Y L N G E V E A I V G 180
181 GGTTTTGAAGCTATGGTTATAGCTCCTTTAGTAATCAAGCGAACTCTCTTAACCTCTGGG
   G F G S Y G Y S S F S N Q A N S L N S G 240
241 GCCAATAACACTAATTTTGGCGTGTATAGCCGTATTTTGGCTAACCAGCATGAATTTGAC
   A N N T N F G V Y S R I F A N Q H E F D 300
301 TTTGAAGCTCAAGGGGCGCTAGGGAGTGATCAATCAAGCTTGAATTTCAAAGCGCTTTA
   F E A Q G A L G S D Q S S L N F K S A L 360
361 TTGCGAGATTTGAATCAAAGCTATAATTACTTAGCCTATAGCGCTGCAACAAGAGCGAGC
   L R D L N Q S Y N Y L A Y S A A T R A S 420
421 TATGGTTATGACTTCGCGTTTTTTAGGAACGCTTTGGTGTTAAACCAAGCGTGGGCGTG
   Y G Y D F A F F R N A L V L K P S V G V 480
481 AGCTATAACCATTTAGGTTCAACCAACTTTAAAAGCAACAGCAATCAAAAAGTGGCTTTG
   S Y N H L G S T N F K S N S N Q K V A L 540
541 AAAAATGGTGCAAGCAGTCAGCATTATTCAACGCTAGTGCTAATGTGAAGCGCGCTAT
   K N G A S S Q H L F N A S A N V E A R Y 600
601 TATTATGGGGACACTTCATACTTCTACATGAACGCTGGAGTTTTACAAGAGTTCGCTAAC
   Y Y G D T S Y F Y M N A G V L Q E F A N 660
661 TTTGGTTCTAGCAATGCGGTGTCTTTAAACACCTTTAAAGTGAATGCTACTCGTAACCCCT
   F G S S N A V S L N T F K V N A T R N P 720
721 TTAAATACCCATGCGAGAGTGATGATGGGTGGGGAATTAAATTAGCTAAAGAAGTGTTT
   L N T H A R V M M G G E L K L A K E V F 780
781 TTGAATTTGGGCTTTGTTTATTTGCACAATTTGATTTCCAATATAGGCCATTTGCTTCC
   L N L G F V Y L H N L I S N I G H F A S 840
841 AATTTAGGAATGAGGTATAGTTTC
   N L G M R Y S F 864
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